Amendments to the Claims

Listing of Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

1. **(Withdrawn – Currently Amended)** A method of regulating the transcription of a gene comprising introducing into a host cell the ~~nucleic acid molecule of claim 5 or a nucleic acid molecule consisting of SEQ ID NO: 1, wherein the nucleic acid molecule has promoter activity~~ expression unit of claim 6 or an expression unit consisting of SEQ ID NO:2, wherein the expression unit has promoter activity.

2. **(Previously Presented)** A method of regulating the expression of a gene comprising introducing into a host cell the expression unit of claim 6 or an expression unit consisting of SEQ ID NO:2.

3-5. **(Cancelled)**

6. **(Currently Amended)** An expression unit comprising a nucleic acid molecule having promoter activity ~~according to claim 5~~, wherein the nucleic acid molecule is selected from the group consisting of

A) a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1;

B) a nucleic acid molecule comprising a nucleotide sequence of at least 90% identity to the nucleotide sequence of SEQ ID NO:1;

C) a nucleic acid molecule which hybridizes with the complement of the nucleotide sequence of SEQ ID NO:1; and

D) a nucleic acid molecule comprising a fragment of the nucleic acid molecule of (A), (B) or (C), wherein the molecule has promoter activity;

wherein the nucleic acid molecule does not consist of SEQ ID NO:1; and wherein said nucleic acid molecule is functionally linked to a nucleic acid sequence which ensures the translation of ribonucleic acids.

7. **(Previously Presented)** An expression unit according to claim 6, comprising an isolated nucleic acid molecule selected from the group consisting of:

E) a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2;

F) a nucleic acid molecule comprising a nucleotide sequence of at least 90% identity to the nucleotide sequence of SEQ ID NO:2;

G) a nucleic acid molecule which hybridizes with the complement of the nucleotide sequence of SEQ ID NO:2; and

H) a nucleic acid molecule comprising a fragment of the nucleic acid molecule of (E), (F) or (G), wherein the molecule has expression activity;

wherein the nucleic acid molecule does not consist of SEQ ID NO:2. with the proviso that the nucleic acid having the sequence SEQ. ID. NO. 2 is excluded.

8. **(Withdrawn – Currently Amended)** A method for altering or causing the transcription rate of genes in microorganisms compared with the wild type by

a) altering the specific promoter activity in the microorganism of endogenous nucleic acids having promoter activity according to claim 6 ~~claim 1~~, which regulate the transcription of endogenous genes, compared with the wild type or

b) regulating the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 6 ~~claim 1~~ or by nucleic acids having promoter activity according to claim 6 ~~claim 1~~ with altered specific promoter activity according to embodiment a), where the genes are heterologous in relation to the nucleic acids having promoter activity.

9. **(Withdrawn - Currently Amended)** The method according to claim 8, wherein the regulation of the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 6 ~~claim 1~~ or by nucleic acids having promoter activity according to claim 6 ~~claim 1~~ with altered specific promoter activity according to embodiment a) is achieved by

b1) introducing one or more nucleic acids having promoter activity according to claim 6 ~~claim 1~~, where appropriate with altered specific promoter activity, into the genome of the microorganism so that transcription of one or more endogenous genes takes place under the control of the introduced nucleic acid having promoter activity according to claim 6 ~~claim 1~~, where appropriate with altered specific promoter activity, or

b2) introducing one or more genes into the genome of the microorganism so that transcription of one or more of the introduced genes takes place under the control of the endogenous nucleic acids having promoter activity according to claim 6 ~~claim 1~~, where appropriate with altered specific promoter activity, or

b3) introducing one or more nucleic acid constructs comprising a nucleic acid having promoter activity according to claim 6 ~~claim 1~~, where appropriate with altered specific promoter activity, and functionally linked one or more nucleic acids to be transcribed, into the microorganism.

10. **(Withdrawn - Currently Amended)** The method according to claim 8 or 9, wherein to increase or cause the transcription rate of genes in microorganisms compared with the wild type

ah) the specific promoter activity in the microorganism of endogenous nucleic acids having promoter activity according to claim 6 ~~claim 1~~, or which regulate the transcription of endogenous genes, is increased compared with the wild type, or

bh) the transcription of genes in the microorganism is regulated by nucleic acids having promoter activity according to claim 6 ~~claim 1~~ or by nucleic acids having increased specific promoter activity according to embodiment a), where the genes are heterologous in relation to the nucleic acids having promoter activity.

11. **(Withdrawn - Currently Amended)** The method according to claim 10, wherein the regulation of the transcription of genes in the microorganism by nucleic acids having promoter activity according to claim 6 ~~claim 1~~ or by nucleic acids having promoter activity

according to claim 6 ~~claim 1~~ with increased specific promoter activity according to embodiment a) is achieved by

bh1) introducing one or more nucleic acids having promoter activity according to claim 6 ~~claim 1~~, where appropriate with increased specific promoter activity, into the genome of the microorganism so that transcription of one or more endogenous genes takes place under the control of the introduced nucleic acid having promoter activity according to claim 6 ~~claim 1~~, where appropriate with increased specific promoter activity, or

bh2) introducing one or more genes into the genome of the microorganism so that transcription of one or more of the introduced genes takes place under the control of the endogenous nucleic acids having promoter activity according to claim 6 ~~claim 1~~, where appropriate with increased specific promoter activity, or

bh3) introducing one or more nucleic acid constructs comprising a nucleic acid having promoter activity according to claim 6 ~~claim 1~~, where appropriate with increased specific promoter activity, and functionally linked one or more nucleic acids to be transcribed, into the microorganism.

12. **(Withdrawn - Currently Amended)** The method according to claim 8 or 9, wherein to reduce the transcription rate of genes in microorganisms compared with the wild type

ar) the specific promoter activity in the microorganism of endogenous nucleic acids having promoter activity according to claim 6 ~~claim 1~~, which regulate the transcription of endogenous genes, is reduced compared with the wild type, or

br) nucleic acids having reduced specific promoter activity according to embodiment a) are introduced into the genome of the microorganism so that the transcription of endogenous genes takes place under the control of the introduced nucleic acid having reduced promoter activity.

13. **(Withdrawn - Currently Amended)** A method for altering or causing the expression rate of a gene in microorganisms compared with the wild type by

c) altering the specific expression activity in the microorganism of endogenous expression units according to claim 6 ~~claim 2~~, which regulate the expression of the endogenous genes, compared with the wild type or

d) regulating the expression of genes in the microorganism by expression units according to claim 6 ~~claim 2~~ or by expression units according to claim 6 ~~claim 2~~ with altered specific expression activity according to embodiment c), where the genes are heterologous in relation to the expression units.

14. **(Withdrawn- Currently Amended)** The method according to claim 13, wherein the regulation of the expression of genes in the microorganism by expression units according to claim 6 ~~claim 2~~ or by expression units according to claim 6 ~~claim 2~~ with altered specific expression activity according to embodiment a) is achieved by

d1) introducing one or more expression units according to claim 6 ~~claim 2~~, where appropriate with altered specific expression activity, into the genome of the microorganism so that expression of one or more endogenous genes takes place under the control of the introduced expression units, or

d2) introducing one or more genes into the genome of the microorganism so that expression of one or more of the introduced genes takes place under the control of the endogenous expression units according to claim 6 ~~claim 2~~, where appropriate with altered specific expression activity, or

d3) introducing one or more nucleic acid constructs comprising an expression unit according to claim 6 ~~claim 2~~, where appropriate with altered specific expression activity, and functionally linked one or more nucleic acids to be expressed, into the microorganism.

15. **(Withdrawn - Currently Amended)** The method according to claim 13 or 14, wherein to increase or cause the expression rate of a gene in microorganisms compared with the wild type

ch) the specific expression activity in the microorganism of endogenous expression units according to claim 6 ~~claim 2~~, which regulate the expression of the endogenous genes, is increased compared with the wild type, or

dh) the expression of genes in the microorganism is regulated by expression units according to claim 6 ~~claim 2~~ or by expression units according to claim 6 ~~claim 2~~ with increased specific expression activity according to embodiment a), where the genes are heterologous in relation to the expression units.

16. **(Withdrawn - Currently Amended)** The method according to claim 15, wherein the regulation of the expression of genes in the microorganism by expression units according to claim 6 ~~claim 2~~ or by expression units according to claim 6 ~~claim 2~~ with increased specific expression activity according to embodiment a) is achieved by

dh1) introducing one or more expression units according to claim 6 ~~claim 2~~, where appropriate with increased specific expression activity, into the genome of the microorganism so that expression of one or more endogenous genes takes place under the control of the introduced expression units, where appropriate with increased specific expression activity, or

dh2) introducing one or more genes into the genome of the microorganism so that expression of one or more of the introduced genes takes place under the control of the endogenous expression units according to claim 6 ~~claim 2~~, where appropriate with increased specific expression activity, or

dh3) introducing one or more nucleic acid constructs comprising an expression unit according to claim 6 ~~claim 2~~, where appropriate with increased specific expression activity, and functionally linked one or more nucleic acids to be expressed, into the microorganism.

17. **(Withdrawn - Currently Amended)** The method according to claim 13 or 14, wherein to reduce the expression rate of genes in microorganisms compared with the wild type

cr) the specific expression activity in the microorganism of endogenous expression units according to claim 6 ~~claim 2~~, which regulate the expression of the endogenous genes, is reduced compared with the wild type, or

dr) expression units with reduced specific expression activity according to embodiment cr) are introduced into the genome of the microorganism so that expression of endogenous genes takes place under the control of the introduced expression units with reduced expression activity.

18. **(Withdrawn)** The method according to claim 8, wherein the genes are selected from the group of nucleic acids encoding a protein from the biosynthetic pathway of proteinogenic and non-proteinogenic amino acids, nucleic acids encoding a protein from the biosynthetic pathway of nucleotides and nucleosides, nucleic acids encoding a protein from the biosynthetic pathway of organic acids, nucleic acids encoding a protein from the biosynthetic pathway of lipids and fatty acids, nucleic acids encoding a protein from the biosynthetic pathway of diols, nucleic acids encoding a protein from the biosynthetic pathway of carbohydrates, nucleic acids encoding a protein from the biosynthetic pathway of aromatic compounds, nucleic acids encoding a protein from the biosynthetic pathway of vitamins, nucleic acids encoding a protein from the biosynthetic pathway of cofactors and nucleic acids encoding a protein from the biosynthetic pathway of enzymes, where the genes may optionally comprise further regulatory elements.

19. **(Withdrawn)** The method according to claim 18, wherein the proteins from the biosynthetic pathway of amino acids are selected from the group of aspartate kinase, aspartate-semialdehyde dehydrogenase, diaminopimelate dehydrogenase, diaminopimelate decarboxylase, dihydrodipicolinate synthetase, dihydrodipicolinate reductase, glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, pyruvate carboxylase, triosephosphate isomerase, transcriptional regulator LuxR, transcriptional regulator LysR1, transcriptional regulator LysR2, malate-quinone oxidoreductase, glucose-6-phosphate deydrogenase, 6-phosphogluconate

dehydrogenase, transketolase, transaldolase, homoserine O-acetyltransferase, cystathionine gamma-synthase, cystathionine beta-lyase, serine hydroxymethyltransferase, O-acetylhomoserine sulfhydrylase, methylenetetrahydrofolate reductase, phosphoserine aminotransferase, phosphoserine phosphatase, serine acetyltransferase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine exporter carrier, threonine dehydratase, pyruvate oxidase, lysine exporter, biotin ligase, cysteine synthase I, cysteine synthase II, coenzyme B12-dependent methionine synthase, coenzyme B12-independent methionine synthase, sulfate adenylyltransferase subunit 1 and 2, phosphoadenosine-phosphosulfate reductase, ferredoxin-sulfite reductase, ferredoxin NADP reductase, 3-phosphoglycerate dehydrogenase, RXA00655 regulator, RXN2910 regulator, arginyl-tRNA synthetase, phosphoenolpyruvate carboxylase, threonine efflux protein, serine hydroxymethyltransferase, fructose-1,6-bisphosphatase, protein of sulfate reduction RXA077, protein of sulfate reduction RXA248, protein of sulfate reduction RXA247, protein OpcA, 1-phosphofructokinase and 6-phosphofructokinase.

20-54. (Cancelled)